

CHIR-0337.ST25.txt  
SEQUENCE LISTING

<110> Covacci, Antonio  
Bugnoli, Massimo  
Telford, John  
Macchia, Giovanni  
Rappuoli, Rino

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<141> 2003-07-08

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<151> 1999-10-01

<150> US 08/471,491  
<151> 1995-06-06

<150> US 08/256,848  
<151> 1994-10-21

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<170> PatentIn version 3.3

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 Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly  
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 115 120 125  
 Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr  
 130 135 140  
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 165 170 175  
 Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala  
 180 185 190  
 Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly  
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 Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp  
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 Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser  
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515

520

525

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 Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu  
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## CHIR-0337.ST25.txt

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Ala	Leu 1160	Val	Leu	Lys	Pro	Ser 1165	Val	Gly	Val	Ser	Tyr 1170	Asn	His	Leu
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## CHIR-0337.ST25.txt

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CHIR-0337.ST25.txt

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gtaaaagaca ctaattctgg ctttacgcaa tttttaacca atgcattttc tacagcatct	3900
tattactgct tggcgagaga aaatgcggag catggaatca agaacgttaa tacaaaaggt	3960
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aaagcgaggg gttttttaat actccttagc agaaatccca atcgtcttta gtatttgga	4080
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gcaaagttac gcctttggag atatgatgtg tgagacctgt agggaatgagc ttggagctca	4200
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acatcagcct aggaagccca atcgtcttta gcggttgggc acttcacctt aaaatatccc	4320
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aagatcaagt tcaaaaaatc atagagcttt tagagcaa atgatcgcgct cttaaccaaa	4560
gaaaaatcag aaaaaccata ggaattatca caccttataa tgcccaaaaa agacgcttgc	4620
gatcagaagt ggaaaaatac ggcttcaaga attttgatga gctcaaaata gacactgtgg	4680
atgcctttca aggtgaagag gcagatatta ttattttatt caccgtgaaa acttggtgta	4740
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cattcttcgc ttcaaacgc tttcataaat ctctctaaag cgctttataa tcaacacaat	4980
acccttatag tgtgagctat agcccccttt tgggaattga gttattttga ctttaaattt	5040
ttattagcgt tacaatttga gccattcttt agcttgtttt tctagccaga tcacatcgcc	5100

## CHIR-0337.ST25.txt

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<210> 5
<211> 1147
<212> PRT
<213> Helicobacter pylori

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<400> 5
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```

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Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Leu Lys Val
20          25          30

```

```
Asp Asn Ala Val Ala Ser Tyr Asp Pro Asp Gln Lys Pro Ile Val Asp
35          40          45

```

```
Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Gly Ile Ser Gln Leu
50          55          60

```

```
Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn
65          70          75          80

```

```
Gln Tyr Phe Ser Asp Phe Ile Asn Lys Ser Asn Asp Leu Ile Asn Lys
85          90          95

```

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Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys Ser Phe Gln Lys Phe
100          105          110

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## CHIR-0337.ST25.txt

Gly Asp Gln Arg Tyr Arg Ile Phe Thr Ser Trp Val Ser His Gln Asn  
 115 120 125  
 Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg Asn Phe Met Glu Asn  
 130 135 140  
 Ile Ile Gln Pro Pro Ile Leu Asp Asp Lys Glu Lys Ala Glu Phe Leu  
 145 150 155 160  
 Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile  
 165 170 175  
 Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu  
 180 185 190  
 Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Thr Gly Gly Asp Trp Leu  
 195 200 205  
 Asp Ile Phe Leu Ser Phe Ile Phe Asp Lys Lys Gln Ser Ser Asp Val  
 210 215 220  
 Lys Glu Ala Ile Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Ile  
 225 230 235 240  
 Ala Thr Thr Thr Thr Asp Ile Gln Gly Leu Pro Pro Glu Ala Arg Asp  
 245 250 255  
 Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met  
 260 265 270  
 Glu Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys  
 275 280 285  
 Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met  
 290 295 300  
 Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly  
 305 310 315 320  
 Gly Asn Gly Gly Pro Gly Ala Arg His Asp Trp Asn Ala Thr Val Gly  
 325 330 335  
 Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr Ile Ile Asn Val His  
 340 345 350  
 Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile

355

360

365

Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser  
 370 375 380  
 Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys Ile Asp Phe Met  
 385 390 395 400  
 Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Glu Lys  
 405 410 415  
 Glu Lys Glu Lys Phe Arg Thr Glu Ile Lys Asp Phe Gln Lys Asp Ser  
 420 425 430  
 Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg Ile Ala Phe Val Ser  
 435 440 445  
 Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr Glu Phe Gly Asn Gly  
 450 455 460  
 Asp Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala  
 465 470 475 480  
 Leu Asp Arg Glu Lys Asn Val Thr Leu Gln Gly Ser Leu Lys His Asp  
 485 490 495  
 Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser  
 500 505 510  
 Lys Asn Pro Asn Lys Gly Val Gly Val Thr Asn Gly Val Ser His Leu  
 515 520 525  
 Glu Val Gly Phe Asn Lys Val Ala Ile Phe Asn Leu Pro Asp Leu Asn  
 530 535 540  
 Asn Leu Ala Ile Thr Ser Phe Val Arg Arg Asn Leu Glu Asp Lys Leu  
 545 550 555 560  
 Thr Thr Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Ile Lys Asp  
 565 570 575  
 Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Thr Leu Asn Phe Asn  
 580 585 590  
 Lys Ala Val Ala Asp Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys  
 595 600 605

Lys Ala Gln Lys Asp Leu Glu Lys Ser Leu Arg Lys Arg Glu His Leu  
 610 615 620  
 Glu Lys Glu Val Glu Lys Lys Leu Glu Ser Lys Ser Gly Asn Lys Asn  
 625 630 635 640  
 Lys Met Glu Ala Lys Ala Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe  
 645 650 655  
 Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr  
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 Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu  
 675 680 685  
 Asn Val Asn Lys Asn Leu Lys Asp Phe Asp Lys Ser Phe Asp Glu Phe  
 690 695 700  
 Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys  
 705 710 715 720  
 Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile  
 725 730 735  
 Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu Phe Lys Asn Gly  
 740 745 750  
 Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser Asp Leu Glu  
 755 760 765  
 Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys Val Thr Asp Lys Val  
 770 775 780  
 Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr Gly Asp Phe  
 785 790 795 800  
 Ser Arg Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe Ser Lys Glu  
 805 810 815  
 Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Ser Leu Asn Ala Arg Lys  
 820 825 830  
 Lys Ser Glu Ile Tyr Gln Ser Val Lys Asn Gly Val Asn Gly Thr Leu  
 835 840 845  
 Val Gly Asn Gly Leu Ser Gln Ala Glu Ala Thr Thr Leu Ser Lys Asn  
 850 855 860

## CHIR-0337.ST25.txt

Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly Asn Phe Asn  
 865 870 875 880  
 Asn Asn Asn Asn Asn Gly Leu Lys Asn Glu Pro Ile Tyr Ala Lys Val  
 885 890 895  
 Asn Lys Lys Lys Ala Gly Gln Ala Ala Ser Leu Glu Glu Pro Ile Tyr  
 900 905 910  
 Ala Gln Val Ala Lys Lys Val Asn Ala Lys Ile Asp Arg Leu Asn Gln  
 915 920 925  
 Ile Ala Ser Gly Leu Gly Val Val Gly Gln Ala Ala Gly Phe Pro Leu  
 930 935 940  
 Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Arg  
 945 950 955 960  
 Asn Gln Glu Leu Ala Gln Lys Ile Asp Asn Leu Asn Gln Ala Val Ser  
 965 970 975  
 Glu Ala Lys Ala Gly Phe Phe Gly Asn Leu Glu Gln Thr Ile Asp Lys  
 980 985 990  
 Leu Lys Asp Ser Thr Lys His Asn Pro Met Asn Leu Trp Val Glu Ser  
 995 1000 1005  
 Ala Lys Lys Val Pro Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr  
 1010 1015 1020  
 Ala Thr Asn Ser His Ile Arg Ile Asn Ser Asn Ile Lys Asn Gly  
 1025 1030 1035  
 Ala Ile Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Pro  
 1040 1045 1050  
 Glu Trp Leu Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val  
 1055 1060 1065  
 Gly Ser Val Pro Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln  
 1070 1075 1080  
 Lys Asn Met Lys Asp Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys  
 1085 1090 1095  
 Leu Asn Asn Ala Val Lys Asp Thr Asn Ser Gly Phe Thr Gln Phe  
 1100 1105 1110



Leu Thr Asn Ala Phe Ser Thr Ala Ser Tyr Tyr Cys Leu Ala Arg  
 1115 1120 1125

Glu Asn Ala Glu His Gly Ile Lys Asn Val Asn Thr Lys Gly Gly  
 1130 1135 1140

Phe Gln Lys Ser  
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<210> 6  
 <211> 546  
 <212> PRT  
 <213> Helicobacter pylori  
 <400> 6

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe  
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Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro  
 20 25 30

Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile  
 35 40 45

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro  
 50 55 60

Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr  
 65 70 75 80

Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr  
 85 90 95

Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro  
 100 105 110

Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn  
 115 120 125

Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr  
 130 135 140

Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu  
 145 150 155 160

Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val  
 165 170 175

## CHIR-0337.ST25.txt

Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met  
 180 185 190  
 Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu  
 195 200 205  
 Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys  
 210 215 220  
 Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met  
 225 230 235 240  
 Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu  
 245 250 255  
 Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile  
 260 265 270  
 Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu  
 275 280 285  
 Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu  
 290 295 300  
 Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly  
 305 310 315 320  
 Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly  
 325 330 335  
 His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile  
 340 345 350  
 Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu  
 355 360 365  
 Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser  
 370 375 380  
 Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser  
 385 390 395 400  
 Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala  
 405 410 415  
 Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp

420  
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 430  
 Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu  
 435 440 445  
 Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn  
 450 455 460  
 Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly  
 465 470 475 480  
 Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val  
 485 490 495  
 Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu  
 500 505 510  
 Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Thr Pro  
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 530 535 540  
 Met Met  
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<210> 7  
 <211> 1838  
 <212> DNA  
 <213> Helicobacter pylori

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 ctccatgacg ctgtcaaagt aaccatgggg ccaagaggca ggaatgtatt gatccaaaaa 180  
 agctatggcg ctccaagcat caccaaagac ggcgtgagcg tggctaaaga gattgaatta 240  
 agttgcccag tagctaacat gggcgctcaa ctcgttaaag aagtagcgag caaaaccgct 300  
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 gctgctgaag cgatcattaa tgagcttaaa aaagcgagca aaaaagtagg cggtaaagaa 480  
 gaaatcacc aagtggcgac catttctgca aactccgac acaatatcg gaaactcatc 540  
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CHIR-0337.ST25.txt

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gagggcaaac cgcttttaat catcgctgaa gacattgagg gcgaagcttt aacgactcta	840
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gacagaagaa aagaaatgct caaagacatc gctattttta cggcggtca agtcattagc	960
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actaaagcgg cggttgaaga aggcattgtg attggtggcg gtgcggctct cattcgcgcg	1320
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cgcgccatta aagccccatt agctcaaatc gctatcaacg ctggttatga tggcggtgtg	1440
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aaagaagaaa aagcgactcc ggcaatgcct gatatgggtg gcatgggcgg tatgggaggc	1680
atgggcggca tgatgtaagc ccgcttgctt tttagtataa tctgctttta aaatcccttc	1740
tctaaatccc cccctttcta aaatctcttt tttggggggg tgctttgata aaaccgctcg	1800
cttgtaaaaa catgcaacaa aaaatctctg ttaagctt	1838

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer oligonucleotide

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<210> 9  
 <211> 12  
 <212> PRT  
 <213> Helicobacter pylori

<400> 9

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<210> 10  
 <211> 5  
 <212> PRT  
 <213> Helicobacter pylori

<400> 10

Glu Pro Ile Tyr Ala  
 1 5

<210> 11  
 <211> 102  
 <212> DNA  
 <213> Helicobacter pylori

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 ccctttgaaa ggcataataa agttgatgat cttagtaagg ta 102

<210> 12  
 <211> 34  
 <212> PRT  
 <213> Helicobacter pylori

<400> 12

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 1 5 10 15

Gly Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser  
 20 25 30

Lys Val

<210> 13  
 <211> 18  
 <212> DNA  
 <213> Helicobacter pylori

<400> 13  
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<210> 14  
 <211> 6  
 <212> PRT  
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<400> 14

Pro Glu Pro Ile Tyr Ala  
 1 5

<210> 15

<211> 9  
 <212> DNA  
 <213> Helicobacter pylori

<400> 15  
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9

<210> 16  
 <211> 3  
 <212> PRT  
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<400> 16

Asp Asp Leu  
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<210> 17  
 <211> 15  
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 <213> Helicobacter pylori

<400> 17

Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val  
 1 5 10 15

<210> 18  
 <211> 45  
 <212> DNA  
 <213> Helicobacter pylori

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45

<210> 19  
 <211> 36  
 <212> DNA  
 <213> Helicobacter pylori

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36

<210> 20  
 <211> 15  
 <212> DNA  
 <213> Helicobacter pylori

<400> 20  
 gaaccattt atgct

15

<210> 21  
 <211> 15  
 <212> DNA  
 <213> Helicobacter pylori

<400> 21

gaacccattt acgct

15

<210> 22  
 <211> 45  
 <212> DNA  
 <213> Helicobacter pylori

<400> 22  
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45

<210> 23  
 <211> 6  
 <212> PRT  
 <213> Helicobacter pylori

<400> 23

Asn Asn Asn Asn Asn Asn  
 1 5

<210> 24  
 <211> 18  
 <212> DNA  
 <213> Helicobacter pylori

<400> 24  
 aataacaata acaataat

18

<210> 25  
 <211> 6  
 <212> PRT  
 <213> Helicobacter pylori

<400> 25

Asn Glu Pro Ile Tyr Ala  
 1 5

<210> 26  
 <211> 6  
 <212> PRT  
 <213> Helicobacter pylori

<400> 26

Glu Glu Pro Ile Tyr Ala  
 1 5

<210> 27  
 <211> 228  
 <212> PRT  
 <213> Helicobacter pylori

<400> 27

Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser  
 1 5 10 15

CHIR-0337.ST25.txt

Asp Leu Glu Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys Val Thr  
20 25 30

Asp Lys Val Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr  
35 40 45

Gly Asp Phe Ser Arg Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe  
50 55 60

Ser Lys Glu Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Ser Leu Asn  
65 70 75 80

Ala Arg Lys Lys Ser Glu Ile Tyr Gln Ser Val Lys Asn Gly Val Asn  
85 90 95

Gly Thr Leu Val Gly Asn Gly Leu Ser Gln Ala Glu Ala Thr Thr Leu  
100 105 110

Ser Lys Asn Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly  
115 120 125

Asn Phe Asn Asn Asn Asn Asn Asn Gly Leu Lys Asn Glu Pro Ile Tyr  
130 135 140

Ala Lys Val Asn Lys Lys Lys Ala Gly Gln Ala Ala Ser Leu Glu Glu  
145 150 155 160

Pro Ile Tyr Ala Gln Val Ala Lys Lys Val Asn Ala Lys Ile Asp Arg  
165 170 175

Leu Asn Gln Ile Ala Ser Gly Leu Gly Val Val Gly Gln Ala Ala Gly  
180 185 190

Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly  
195 200 205

Leu Ser Arg Asn Gln Glu Leu Ala Gln Lys Ile Asp Asn Leu Asn Gln  
210 215 220

Ala Val Ser Glu  
225

<210> 28  
<211> 685  
<212> DNA  
<213> Helicobacter pylori



## CHIR-0337.ST25.txt

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 gcggtatcag tggctaaagc aacgggtgat ttcagtaggg tagagcaagc gttagccgat 180  
 ctcaaaaatt tctcaaagga gcaattggcc caacaagctc aaaaaaatga aagtctcaat 240  
 gctagaaaaa aatctgaaat atatcaatcc gttaagaatg gtgtgaatgg aaccctagtc 300  
 ggtaatgggt tatctcaagc agaagccaca actcttttcta aaaacttttc ggacatcaag 360  
 aaagagttga atgcaaaact tggaaatttc aataacaata acaataatgg actcaaaaac 420  
 gaacccatatt atgctaaagt taataaaaag aaagcagggc aagcagctag ccttgaagaa 480  
 ccattttacg ctcaagttgc taaaaaggta aatgcaaaaa ttgaccgact caatcaata 540  
 gcaagtgggt tgggtgttgt agggcaagca gcgggcttcc ctttgaaaag gcatgataaa 600  
 gttgatgatc tcagtaaggt agggctttca aggaatcaag aattggctca gaaaattgac 660  
 aatctcaatc aagcggatc agaag 685

<210> 29  
 <211> 699  
 <212> DNA  
 <213> Helicobacter pylori

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